

IntelliGenetics

FastDB - Fast Pairwise Comparison of Sequences  
Release 5.4

Results file us-09-967-30i-2.res made by bobyren on Wed 16 Jul 2003 15:58:51-PDT.

Query sequence being compared: US-09-967-301-2 (1-235)  
 Number of sequences searched: 3  
 Number of scores above cutoff: 3

Results of the initial comparison of US-09-967-301-2 (1-238) with:  
File : US09967301.pdf

[illegible]

Sequence Name	Description	Length	Score	Seq. Frame	Init. Opt.
1					
2					
3					
4					
5					
6					
7					
8					
9					
10					
11					
12					
13					
14					
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89					
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92					
93					
94					
95					
96					
97					
98					
99					
100					

```

220      230      X
3. US-09-967-301-2 (1-238)
   US-09-967-301-3 Sequence 3, Application US/C9967301
Initial Score = 237 Optimized Score = 237 Significance = 0.00
Residue Identity = 98% Matches = 235 Mismatches = 3
Caps = 0 Conservative Substitutions = 0
X      10      20      30      40      50      60      70
MSKGEELFTGVVPIVLVDLDGVNKHKFSVSGEGDATYCKLTLPKICTTGKLPVPMPTLVTTESYGVQCF
|||||
MSKGEELFTGVVPIVLVDLDGVNKHKFSVSGEGDATYCKLTLPKICTTGKLPVPMPTLVTTESYGVQCF
X      10      20      30      40      50      60      70
RYPDMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFECDTLVNRILKLGIDFKEDGNILGHKLEYN
|||||
RYPDMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFECDTLVNRILKLGIDFKEDGNILGHKLEYN
80      90      100      110      120      130      140
YNSHNYIMADKQKNGIKVNFKRHNIEDGSGVOLADHYOONTPIGGPVLIPDNHYLSTOSALS KDPNEKRD
|||||
YNSHNYIMADKQKNGIKVNFKRHNIEDGSGVOLADHYOONTPIGGPVLIPDNHYLSTOSALS KDPNEKRD
150      160      170      180      190      200      210
HNVLLFEVTAAGITHGMDELYK
|||||
HNVLLGEVTAAGITHGMDELYK
220      230      X
```



220 230 X

3. US-09-967-301-3 (1-238);  
US-09-967-301-2 Sequence 2, Application US/09967301

Initial Score = 237 Optimized Score = 237 Significance = 0.00  
Residue Identity = 98% Matches = 235 Mismatches = 3  
Gaps = 0 Conservative Substitutions = 0

X 10 20 30 40 50 60 70  
MSKGELFTGVVPIILVELDGVNGHKFVSVEGEGDATYKLTLPFICTTGKLPVPWPTLVTLTSLSYGVQCF  
|||||  
MSKGELFTGVVPIILVELDGVNGHKFVSVEGEGDATYKLTLPFICTTGKLPVPWPTLVTLTSLSYGVQCF  
X 10 20 30 40 50 60 70

80 90 100 110 120 130 140  
RYPDHMKRHDFPKSAMPEGYVQERTIFFKDDGNKYKTRAFVKPEGGTLVNRLEKCIDPKEDGNILGHKLEYN  
|||||  
RYPDHMKRHDFPKSAMPEGYVQERTIFFKDDGNKYKTRAFVKPEGGTLVNRLEKCIDPKEDCNILGHKLEYN  
80 90 100 110 120 130 140

150 160 170 180 190 200 210  
YNSHNYYIMADKQKNGIKVNFIRHNIEDGVSQVLAADHYOONTPIGCGPVLLPDNHYLSTQSALS KDPNEKPT  
|||||  
YNSHNYYIMADKQKNGIKVNFIRHNIEDGVSQVLAADHYOONTPIGCGPVLLPDNHYLSTQSALS KDPNEKPT  
150 160 170 180 190 200 210

220 230 X  
HNVLLGFVTAAGITHGMDELYK  
|||||  
HNVLLGFVTAAGITHGMDELYK  
220 230 X